622

572 3 522

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alignment_block:
US-09-866-034-2 x HSU31875
                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
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AUTHORS
TITLE
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ACCESSION
VERSION
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MEDLINE
REPERENCE
AUTHORS
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ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCUS HSU31875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_pr:HSU31875
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Ratio:
Percent Similarity:
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       10 CysAlaArgAlaTrpAsnSerValArgMetAlaSerSerGlyMetThrAr 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAACATCATCAGCTGCAGAGGATTGGGGAGTCAGAGGACTGTGCAGGAAT 743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTTCAGCAAAGTGTTTCATGGGAATGAGTCTCTCTGGAAGAACTTCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gabrielli,F.
Direct Submission
Submitted (19-JUL-1995) Franco Gabrielli, Physiology and Submitted (19-JUL-1995) Franco Gabrielli, Physiology and Biochemistry, University of Pisa, Via Roma 55, Pisa 56126,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1442)

Gabrielli,F., Donadel,G., Bensi,G., Heguy,A. and Melli,M.

A nuclear protein, synthesized in growth-arrested human hepatoblastoma cells, is a novel member of the short-chain alcohol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Hep27 protein mRNA, complete U31875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dehydrogenase family
Eur. J. Blochem. 232 (2), 473-477 (1995)
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ENRRCAVILVSSIAANNPVVALGVYNVSKTALLGLTRTLALELAPKDIRVNCVVPGII
                                                                                                                                824.50
3.569
87.833
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STRL*
                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to Streptomyces violaceoruber granaticin polyketide synthase putative ketoacyl, Swiss-Prot Accession Number P16542"
                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
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                                                                                                                                                                                                                                                       369
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                                              from: 1
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Gaps: 2
Percent Identity: 61.597
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                                                                                         DEFINITION
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LOCUS AY069779
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     ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                               260
                                                                                                                                                                                                                                                                             243 lyGluProGluAspCysAlaGlyIleValSerPheLeuCysSerGluAsp
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1020 CTAGAACACTGGCATTGGAGCTGGCCCCCAAGGACATCCGGGTAAACTGC 1069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 eMetAspValThrGluGluValTrpAspLySThrLeuAspIleAsnValL
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773 GTCGACTTCCTGGTGTGCAGCGCAGGGGTCAACCCTCTGGTAGGGAGCAC 822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 gArgAspProLeuAlaAsnLysValAlaLeuValThrAlaSerThrAspG
                                                                                                                                                                                      AlaSerTyrIleThrGlyGluThrValValValGlyGly 272
                                                                                                                                                                                                                                                             GGGAGTCAGAGGACTGTGCAGGAATCGTGTCCTTCCTGTGCTCTCCAGAT
                                                                                                                                                                                                                                                                                                                                                  pLysGluLysGluGluSerMetLysGluThrLeuArgIleArgArgLeuG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ...AGGGTGCTGTCATCCTGGTCTCTTCCATTGCAGCTTATAATCCAGT
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                                                                      Drosophila melanogașter SD02021 full length cDNA.
AY069779
Drosophila melanogașter
                        fruit
                                       FLI_CDNA
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143

772

722 93

1219

INV 17-DEC-2001